

FIGURE 1

1 ATGTCAGTGGAGCCATGAGCAAGGAGTGGGAGGGCAGTTGGGCTTGGAGCGGCAGC 60
61 GGTGCCAGGTACGGAGGAAGACCCCTTCCCGACTGCGGAGCTTGGCTCCGGGACAA 120
121 GGTGGCAGGCCTGGAGGCTGCCGACAGCTGCGTGGGTGGAGGGAGCTCAGCTCGGTTG 180
181 TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCTCGCTGCTGCCCACTGGT 240
241 CCCAATGCCAGCAACACTCTGATGGCCCCGATAACCTCACCTCAGCAGGATCACCTCCT 300
301 CGCACGGGAGCATCTCCTACATCAACATCATCATGCTTCCGCTTCCGACCATCTGC 360
361 CTCTGGGCATCATCGGAACCTCACGGTCATCTCGCGTCTGTAAGAAAGTCCAAAGCTG 420
421 CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC 480
481 TTTCTCTGGGCATGCCCTTCATGATCCACAGCTCATGGGCAATGGGTGTGGCACTTT 540
541 GGGGAGACCATGTGCACCCCTCATACGGCCATGGATGCCAATAGTCAGTTCAACGACAC 600
601 TACATCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 720
661 ACGAAGTCCGGRAGCCCTCTGTGGCCACCTGTGTGATCGCCTCTGTGGGCCCTCTCC 780
721 TTTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCCAGGAGTGCA 840
781 GTGGCTGGGCATACGCCCTGCCAACCCAGACACTGACCTCTACTGGTTCAACCTGTAC 900
841 CAGTTTCTCGGCTTTGCCCTTGGCTTGTGTGTCATCACAGCCGCATACGTGAGGATC 960
901 CTGAGCGCATAGCTCCTCAGTGGCCCCGCCCTCCAGCGCAGCATCCGGTGGCGACA 1020
961 AAGAGGTGACCCGCACAGCCATCGCCATCTGTCTGGTCTTCTTTGTGTGGGACCC 1080
1021 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCGCCCCGACCCCTCACCTTTGTCTAC 1140
1081 TTATACAATCGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCTCAACCCCTTTGTGTAC 1200
1141 ATCGTCTCTGTGAGACGTTCCGCAACGCTTGGTCTGTGGTGAAGCCTGCAGCCCCAG 1260
1201 GGGCAGCTTCGCGCTGTACAGCAACGCTCAGACGGCTCAGGAGGAGGAGCAGAAAGCAAA 1269
1261 GGCACCTGA

3/27

FIGURE 3

1 M S V G A M K K G V G R A V G L G G G S 20
 21 G C Q A T E E D P L P D C G A C A P G Q 40
 41 G G R R W R L P Q P A W V E G S S A R L 60
 61 W E Q A T G T G W M D L E A S L L P T G 80
 81 P N A S N T S D G P D N L T S A G S P P 100
 101 R T G S I S Y I N I I I M P S V F G T I C 120
 121 L L G I I G N S T V I F A V V K K S K L 140
 141 H W C N N V P D I F I I N L S V V D L L 160
 161 F L L G M P F M I H Q L M G N G V W H F 180
 181 G E T M C T L I T A M D A N S O F T S T 200
 201 Y I L T A M A I D R Y L A T V H P I S S 220
 221 T K F R K P S V A T L V I C L L W A L S 240
 241 F I S I T P V W L Y A R L I P F P G G A 260
 261 V G C G I R L P N P D T D L Y W F T L Y 280
 281 Q F F L A F A L P F V V I T A A Y V R I 300
 301 L Q R M T S S V A P A S Q R S I R L R T 320
 321 K R V T R T A I A I C L V F F V C W A P 340
 341 Y Y V L O L T O L S I S R P T L T F V Y 360
 361 L Y N A A I S L G Y A N S C L N P F V Y 380
 381 I V L C E T F R K R L V L S V K P A A Q 400
 401 G Q L R A V S N A Q T A D E E R T E S K 420
 421 G T 422

105070.226666

FIGURE 4

1	GCAGCGCCTGCACGGCTGCATGGATCTGCAACCTCGTTGCTGTCCACTGGCCCCAA	60
61	TGCCAGCAACATCTCGATGGCAGGATAATCTCACATTGCCGGGTCACCTCTCGCAC	120
121	AGGAGTGTCTCTACATCAACATCATATGCCTTCCGTGTTGGTACCATCTGTCTCCT	180
181	GGGATCGTGGGAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG	240
241	GTGAGCAACGTCCTCCGACATCTTCATCATCAACCTCTCTGTGGATCTGCTCTTCCT	300
301	GCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGGAACGGCGCTGCGCACTTTGGGA	360
361	AACATGTGACCCCTCATCAAGCCATGGACGCAACAGTCAGTTCATAGCACCTACAT	420
421	CTTCACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCA	480
481	GTTCGGGAAGCCCTCCATGGCCACCCCTGGTGATCTGCTCCTGTGGGCGCTCTCTTCAT	540
541	CAGTATCACCCCTGTGTGGCTACGCCAGGCTCATCCCTTCCCAGGGGGTGTGTGGG	600
601	CTGTGGCATCCGCCCTGCCAAACCCGGACATGACCTCTACTTGGTTCACTCTGTACCA	660
661	TTTCTTGGCCTTTGCCCTTCCGTTTGGGTCAITACCCGCGCATACGTGAAATACTACA	720
721	GCGATGACCTCTTCGGTGGCCCCAGCTCCCAAGCAGATCCGGCTTCGGACAAAGAG	780
781	GGTGACCCGACGGCCATTGCCATCTGTCTGGTCTCTTTGTGTGGGACCCCTACTA	840
841	TGTCTGACGTGACCCAGCTGTCCATCAGCGGCCGACCCCTCACGTTTGTCTACTTGA	900
901	CAACGCGGCATCAGTTTGGGTATGCTAACAGTGCCTGAACCCCTTTGTGTACATAGT	960
961	GCTCTGTGAGACCTTTCGAAACGCTTGGTGTTCAGTGAGCCTGCAGCCAGGGGCA	1020
1021	GCTCCGACCGTCAGCAACGCTCAGACAGTGTAGGAGAGGACAGAAAGCAAGGCAC	1080
1081	CTGACAAATCCCCAGTCGCCTCAAAGTCAGGCCACCCCATCAAAACCGTGGGGAGAGATAC	1140
1141	TGAGATTAAACCCAGGCTACCCCTGGGAGAATGCAGAGGCTGGAGGCTGGGGCTTGTAG	1200
1201	CAACCACATTCAC	1214

5/27

FIGURE 5

1	M	D	L	Q	T	S	L	P	G	S	V	D	L	L	F	G	E	T	M	C	T	L	I	T	20
21	Q	D	N	L	T	L	P	G	T	I	C	L	H	W	C	S	N	V	P	D	I	80			
41	I	I	M	P	S	V	F	G	K	S	K	L	L	F	G	E	T	M	C	T	L	I	T	40	
61	V	I	F	A	V	V	K	K	S	K	L	L	F	G	E	T	M	C	T	L	I	T	60		
81	F	I	I	N	L	S	V	D	L	L	F	G	E	T	M	C	T	L	I	T	100				
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	T	M	C	T	L	I	T	120				
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	L	T	A	M	T	I	D	140				
141	R	Y	L	A	T	V	H	P	I	S	S	T	K	F	R	K	P	S	M	A	160				
161	T	L	V	I	C	L	W	A	L	S	F	I	S	I	T	P	V	W	L	180					
181	Y	A	R	L	I	P	F	G	G	A	V	G	C	G	I	R	L	P	N	200					
201	P	D	T	D	L	Y	W	F	T	L	Y	Q	F	F	L	A	F	A	L	P	220				
221	F	V	V	I	T	A	Y	V	K	I	L	Q	R	M	T	S	S	V	A	240					
241	P	A	S	Q	R	S	I	R	L	R	T	K	R	V	T	R	T	A	I	A	260				
261	I	C	L	V	F	F	V	C	W	A	P	Y	Y	V	L	Q	L	T	Q	L	280				
281	S	I	S	R	P	T	L	T	F	V	Y	L	Y	N	A	A	I	S	L	G	300				
301	Y	A	N	S	C	L	N	P	F	V	Y	I	V	L	C	E	T	F	R	K	320				
321	R	L	V	L	S	V	K	P	A	A	Q	G	Q	L	R	T	V	S	A	340					
341	Q	T	A	D	E	E	R	T	E	S	K	G	T	*						354					

FIGURE 6

IP release in MCH1- and
mock-transfected Cos-7 cells

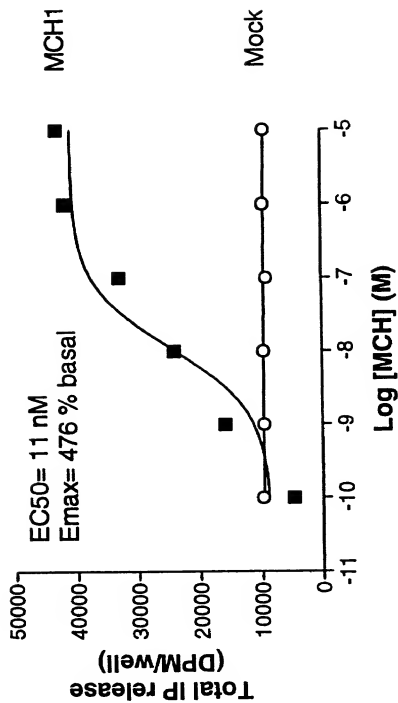
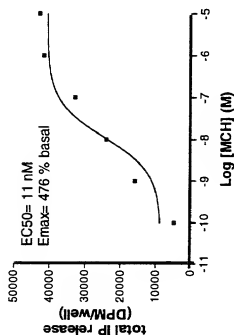
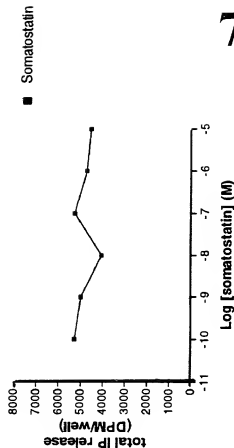


FIGURE 7

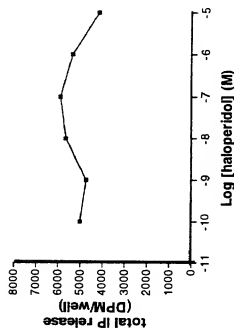
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98



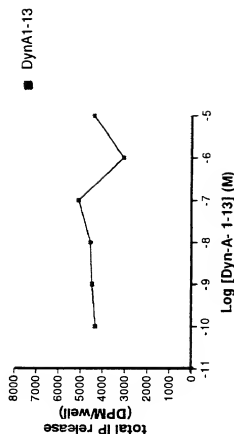
IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98



IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98



IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98

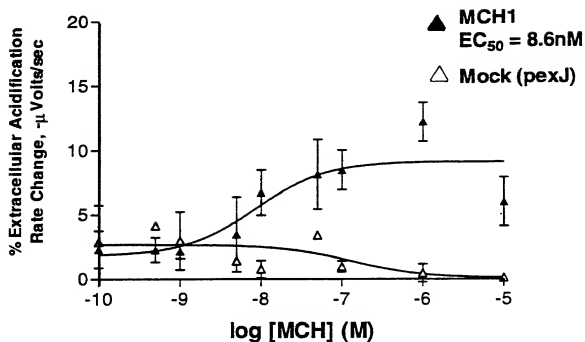


7/27

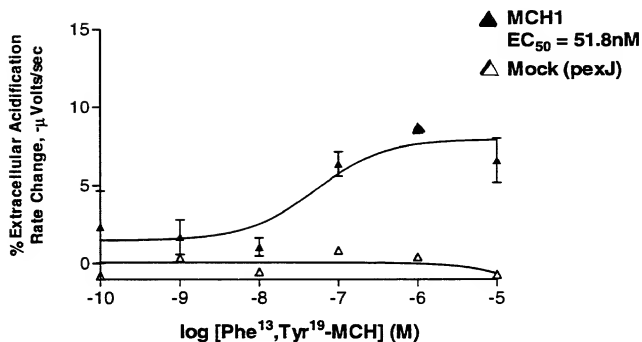
FIGURE 8

8/27

Microphysiometer Response
CHO cells



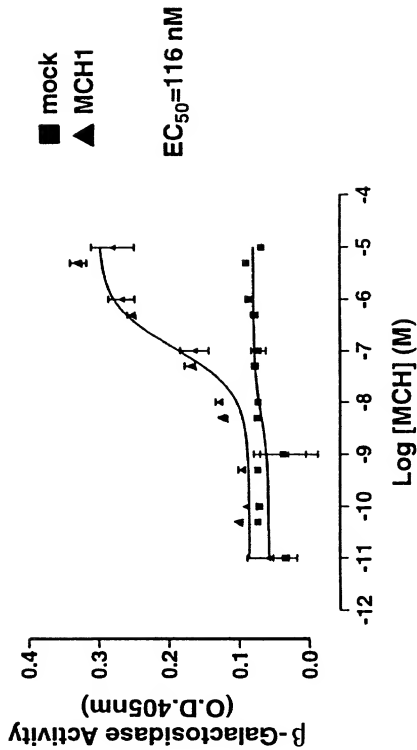
Microphysiometer Response
CHO cells



9/27

FIGURE 9

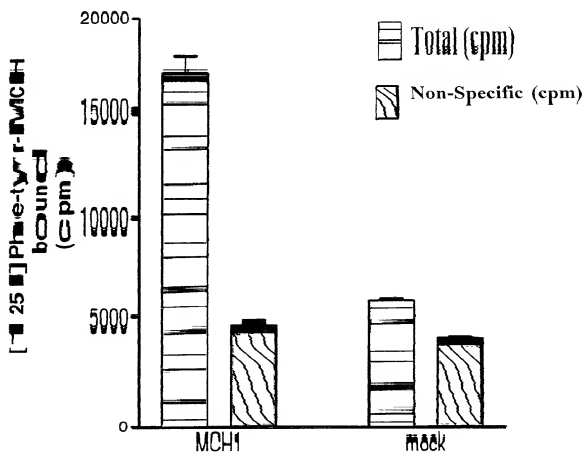
Agonist-Mediated c-fos- β -gal
Activity in Cos-7 Cells



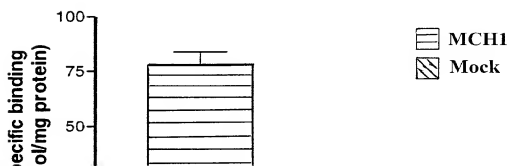
10/27

FIGURE 10

[125I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells



[125I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells



11/27

FIGURE 11

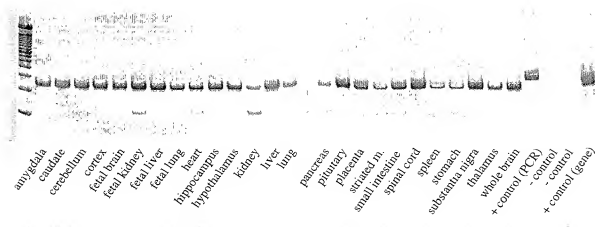


FIGURE 12

TL231	1	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	40
R106		MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	
R114		MSVGAaKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	
B0120		~~~~~	~~~~~	~~~~~	~~~~~	

TL231	41	GRRRWRLPQP	AWVEGSSARL	WEQATGTGWM	DLEASLLPTG	80
R106		GRRRWRLPQP	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG	
R114		GRRRWRLPQP	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG	
B0120		~~~~~	~~~~~	~~~~~M	DLEASLLPTG	

TL231	81	PNASNTSDG?	100	DNLTSAGSP?
R106		PNASNTSDG?		DNLTSAGSP?
R114		PNASNTSDG?		DNLTSAGSP?
B0120		PNASNTSDG?		DNLTSAGSP?

13/27

FIGURE 13

1	M	S	V	G	A	M	K	K	G	V	G	R	A	V	G	L	G	G	G	S	20
21	G	C	Q	A	T	E	E	D	P	L	P	D	C	G	A	C	A	P	G	Q	40
41	G	G	R	R	W	R	L	P	Q	P	A	W	V	E	G	S	S	A	R	L	60
61	W	E	Q	A	T	G	T	G	W	A	D	L	E	A	S	L	L	P	T	G	80
81	P	N	A	S	N	T	S	D	G	P	D	N	L	T	S	A	G	S	P	P	100
101	R	T	G	S	I	S	Y	I	N	I	I	M	P	S	V	F	G	T	I	C	120
121	L	L	G	I	I	G	N	S	T	V	I	F	A	V	V	K	K	S	K	L	140
141	H	W	C	N	N	V	P	D	I	F	I	I	N	L	S	V	V	D	L	L	160
161	F	L	L	G	M	P	F	M	I	H	Q	L	M	G	N	G	V	W	H	F	180
181	G	E	T	M	C	T	L	I	T	A	M	D	A	N	S	Q	E	T	S	T	200
201	Y	I	L	T	A	M	A	I	D	R	Y	L	A	T	V	H	P	I	S	S	220
221	T	X	F	R	K	P	S	V	A	T	L	V	I	C	L	L	W	A	L	S	240
241	F	I	S	I	T	P	V	W	L	Y	A	R	L	I	P	F	P	G	G	A	260
261	V	G	C	G	I	R	L	P	N	P	D	T	D	L	Y	W	F	T	L	Y	280
281	Q	F	F	L	A	F	A	L	F	F	V	V	I	T	A	A	Y	V	R	I	300
301	L	Q	R	M	T	S	S	V	A	P	A	S	Q	R	S	I	R	L	R	T	320
321	K	R	V	T	R	T	A	I	A	I	C	L	V	F	F	V	C	W	A	P	340
341	Y	Y	V	L	Q	L	T	Q	L	S	I	S	R	P	T	L	T	F	V	Y	360
361	L	Y	N	A	A	I	S	L	G	Y	A	N	S	C	L	N	P	F	V	Y	380
381	I	V	L	C	E	T	F	R	K	R	L	V	L	S	V	K	P	A	A	Q	400
401	G	Q	L	R	A	V	S	N	A	Q	T	A	D	E	E	R	T	E	S	K	420
421	G	.																		422	

00000722 070501

14/27

FIGURE 14

1	M	S	V	G	A	A	K	K	G	V	G	R	A	V	G	L	G	G	G	S	20
21	G	C	Q	A	T	E	E	D	P	L	P	D	C	G	A	C	A	P	G	Q	40
41	G	G	R	R	W	R	L	P	Q	P	A	W	V	E	G	S	S	A	R	L	60
61	W	E	Q	A	T	G	T	G	W	A	D	L	E	A	S	L	L	P	T	G	80
81	P	N	A	S	N	T	S	D	G	P	D	N	L	T	S	A	G	S	P	P	100
101	R	T	G	S	I	S	Y	I	N	I	I	M	P	S	V	F	G	T	I	C	120
121	L	L	G	I	I	G	N	S	T	V	I	F	A	V	V	K	K	S	K	L	140
141	H	W	C	N	N	V	P	D	I	F	I	I	N	L	S	V	V	D	L	L	160
161	F	L	L	G	M	P	F	M	I	H	Q	L	M	G	N	G	V	W	H	F	180
181	G	E	T	M	C	T	L	I	T	A	M	D	A	N	S	Q	F	T	S	T	200
201	Y	I	L	T	A	M	A	I	D	R	Y	L	A	T	V	H	P	I	S	S	220
221	T	K	F	R	K	P	S	V	A	T	L	V	I	C	L	L	W	A	L	S	240
241	F	I	S	I	T	P	V	W	L	Y	A	R	L	I	P	F	P	G	G	A	260
261	V	G	C	G	I	R	L	P	N	P	D	T	D	L	Y	W	F	T	L	Y	280
281	Q	F	F	L	A	F	A	L	P	F	V	V	I	T	A	A	Y	V	R	I	300
301	L	Q	R	M	T	S	S	V	A	P	A	S	Q	R	S	I	R	L	R	T	320
321	K	R	V	T	R	T	A	I	A	I	C	L	V	F	F	V	C	W	A	P	340
341	Y	Y	V	L	Q	L	T	Q	L	S	I	S	R	P	T	L	T	F	V	Y	360
361	L	Y	N	A	A	I	S	L	G	Y	A	N	S	C	L	N	P	F	V	Y	380
381	I	V	L	C	E	T	F	R	K	R	L	V	L	S	V	K	P	A	A	Q	400
401	G	Q	L	R	A	V	S	N	A	Q	T	A	D	E	E	R	T	E	S	K	420
421	G	T																		422	

00000772 070001

15/27

FIGURE 15

1	M	D	L	E	A	S	L	L	P	T	G	P	N	A	S	N	T	S	D	G	20
21	P	D	N	L	T	S	A	G	T	P	P	R	T	G	S	I	S	Y	I	N	40
41	I	I	M	P	S	V	F	G	T	I	C	L	L	G	I	I	G	N	S	T	60
61	V	I	F	A	V	V	K	K	S	K	L	H	N	C	N	N	V	P	D	I	80
81	F	I	I	N	L	S	V	V	D	L	L	F	L	L	G	M	P	F	M	I	100
101	H	Q	L	M	G	N	G	V	W	H	F	G	E	T	M	C	T	L	I	T	120
121	A	M	D	A	N	S	Q	F	T	S	T	Y	I	L	T	A	M	A	I	D	140
141	R	Y	L	A	T	V	H	P	I	S	S	T	K	F	R	K	P	S	V	A	160
161	T	L	V	I	C	L	L	W	A	L	S	F	I	S	I	T	P	V	W	L	180
181	V	A	R	L	I	P	F	P	G	G	A	V	G	C	G	L	I	F	A	L	200
201	P	D	T	D	L	Y	W	F	T	L	Y	Q	F	F	L	A	F	A	L	P	220
221	F	V	V	I	T	A	A	Y	V	R	I	L	Q	R	M	T	S	S	V	A	240
241	P	A	S	Q	R	S	I	R	L	R	T	K	R	V	T	R	T	A	I	A	260
261	I	C	L	V	F	F	V	C	W	A	P	Y	Y	V	L	Q	I	T	Q	L	280
281	S	I	S	R	F	T	L	T	F	V	Y	L	Y	N	A	A	I	E	L	G	300
301	Y	A	N	S	C	L	N	P	F	V	Y	I	V	L	C	E	T	F	R	K	320
321	R	L	V	L	S	V	K	P	A	A	Q	G	Q	L	R	A	V	S	N	A	340
341	Q	T	A	D	E	E	R	T	E	S	K	G	T								353

09899732-070501

FIGURE 16

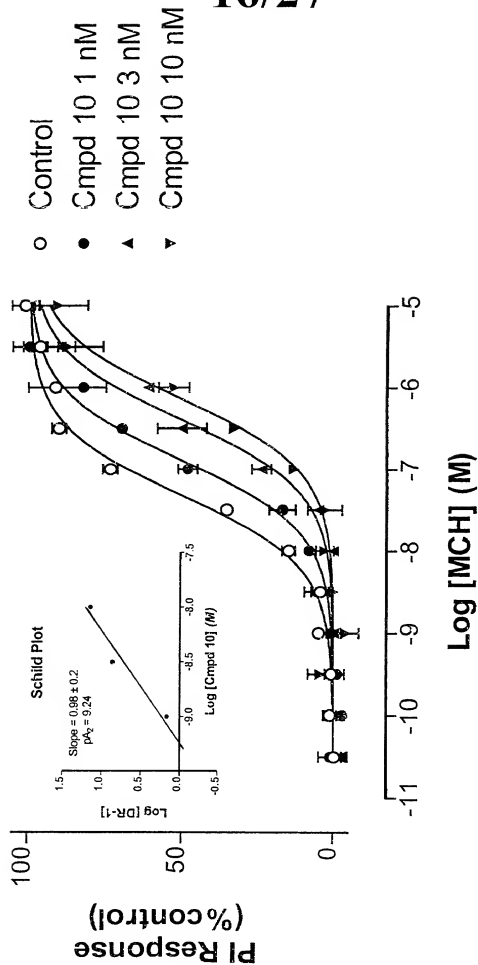
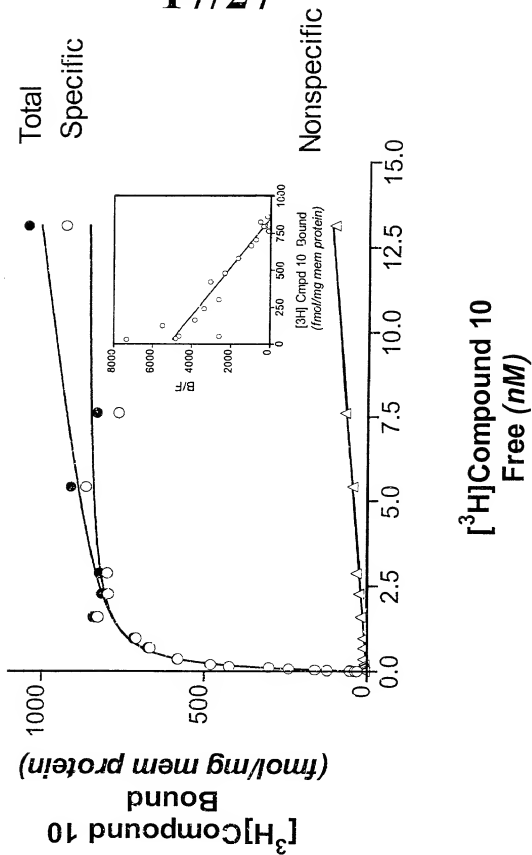
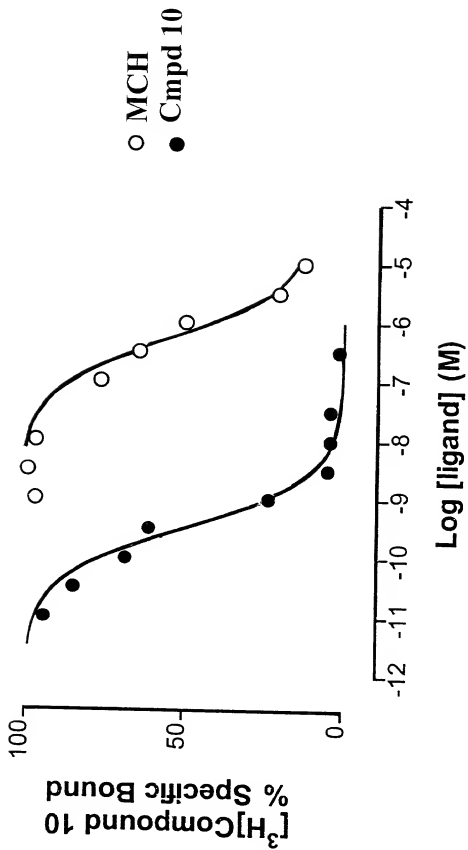


FIGURE 17



18/27

FIGURE 18



19/27

FIGURE 19

**Total MCH1
Receptor Binding**

A



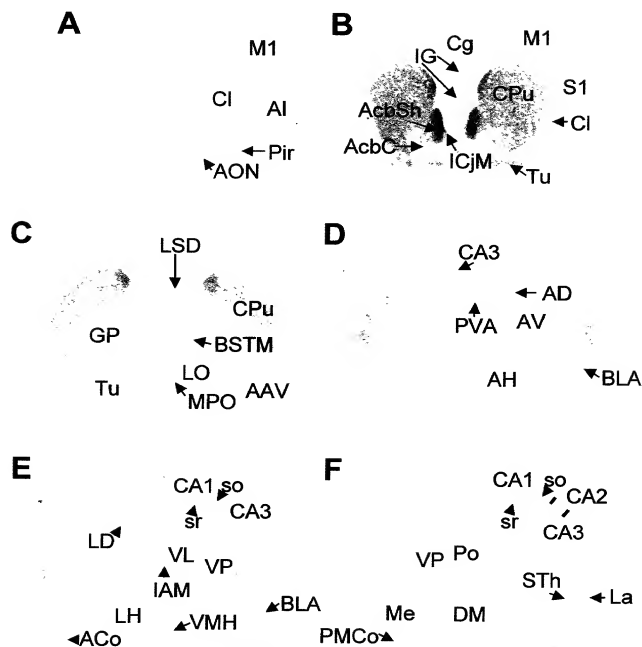
Nonspecific binding

B

09899732-070501

20/27

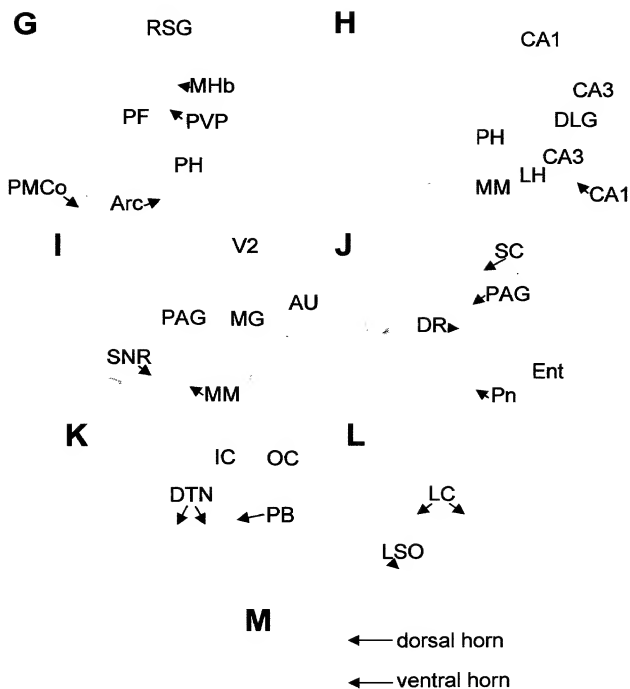
FIGURE 20A



09899732.070501

21/27

FIGURE 20B



09899732-07501

22/27

FIGURE 21

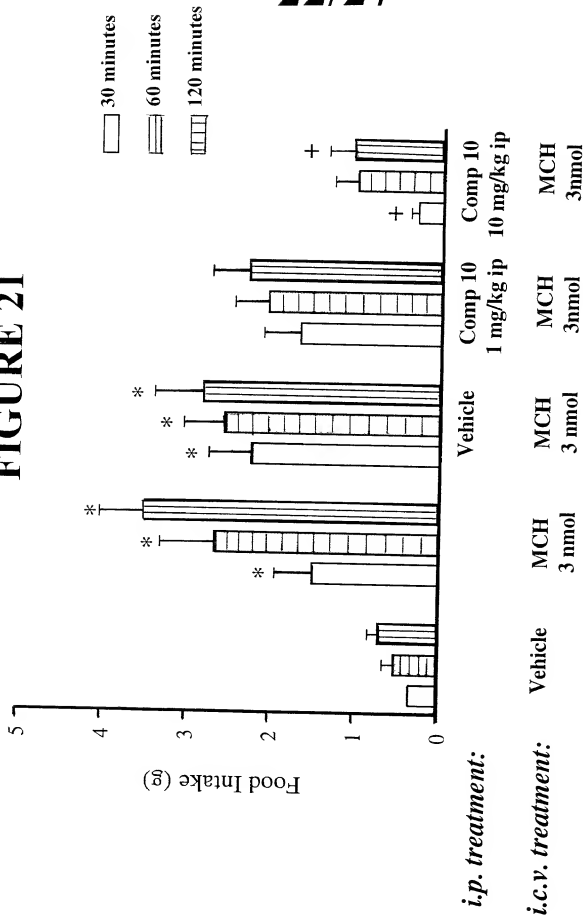
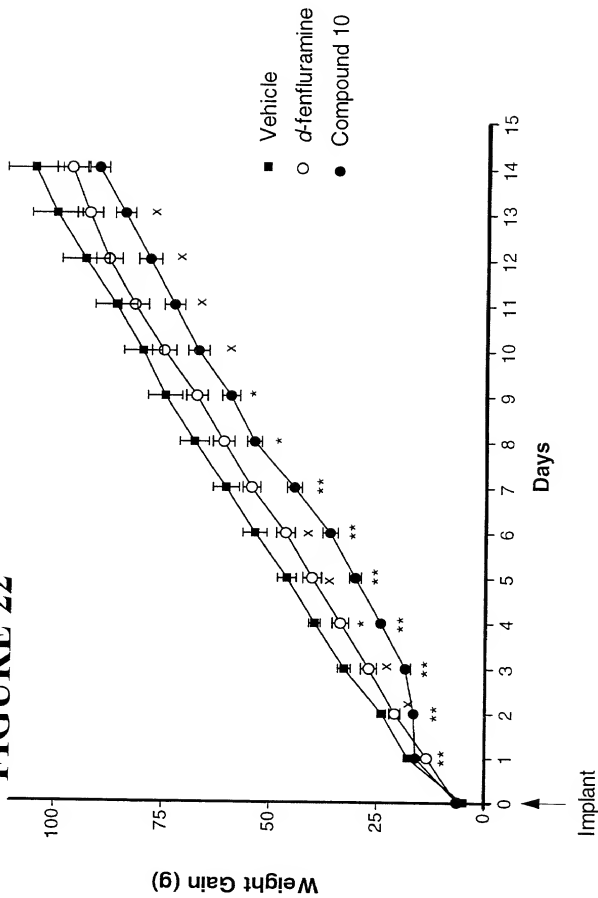
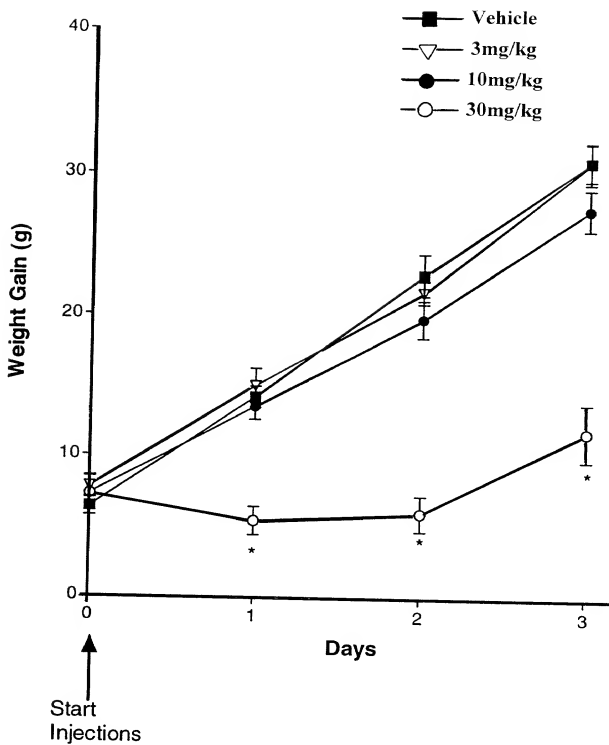


FIGURE 22



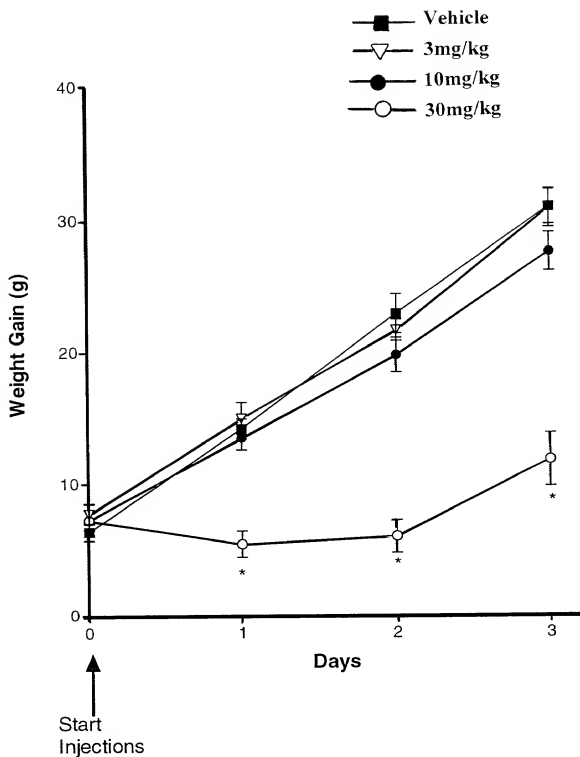
24/27

FIGURE 23



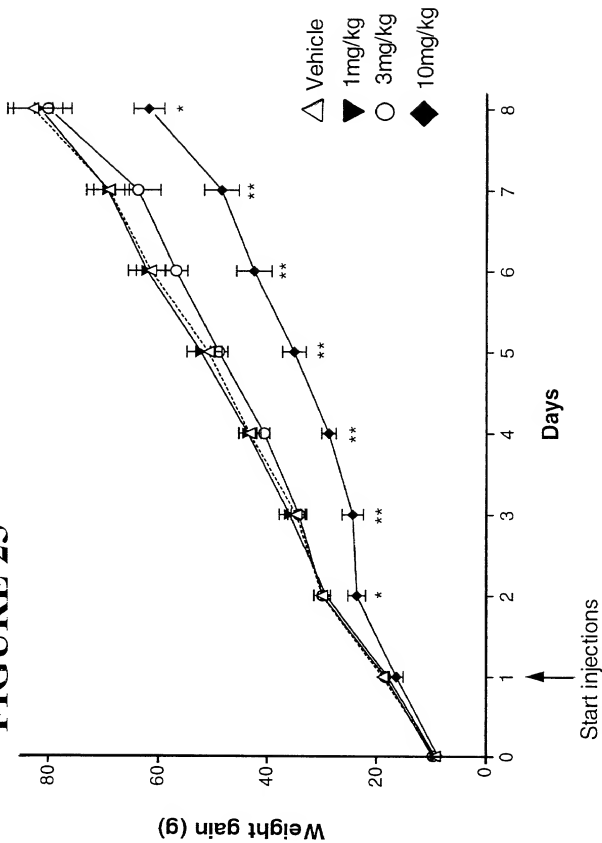
25/27

FIGURE 24



26/27

FIGURE 25



27/27

FIGURE 26

